SEQUENCE LISTING

<110> TRIEBEL, FREDERIC

<120> MOLECULES BINDING TO GLU-PRO MOTIFS, THERAPEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR APPLICATIONS

<130> 1057-04

<140>
<141>

<150> PCT/IB02/04240
<151> 2002-09-17

<150> EP 01402406.1
<151> 2001-09-19

<160> 10

<170> PatentIn version 3.2

<210> 1
<211> 372
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(372)
<223> LAP protein

<400> 1

```
Met Arg Lys Leu Gln Lys Glu Arg Lys Val Phe Glu Lys Tyr Thr Thr
1               5                  10                  15

Ala Ala Arg Thr Phe Pro Asp Lys Lys Glu Arg Glu Glu Ile Gln Thr
            20                  25                  30

Leu Lys Gln Gln Ile Ala Asp Leu Arg Glu Asp Leu Lys Arg Lys Glu
        35                  40                  45

Thr Lys Trp Ser Ser Thr His Ser Arg Leu Arg Ser Gln Ile Gln Met
    50                  55                  60

Leu Val Arg Glu Asn Thr Asp Leu Arg Glu Glu Ile Lys Val Met Glu
65                  70                  75                  80

Arg Phe Arg Leu Asp Ala Trp Lys Arg Ala Glu Ala Ile Glu Ser Ser
                85                  90                  95

Leu Glu Val Glu Lys Lys Asp Lys Leu Ala Asn Thr Ser Val Arg Phe
            100                 105                 110

Gln Asn Ser Gln Ile Ser Ser Gly Thr Gln Val Glu Lys Tyr Lys Lys
        115                 120                 125
```

```
Asn Tyr Leu Pro Met Gln Gly Asn Pro Pro Arg Arg Ser Lys Ser Ala
    130                 135                 140

Pro Pro Arg Asp Leu Gly Asn Leu Asp Lys Gly Gln Ala Ala Ser Pro
145                 150                 155                 160

Arg Glu Pro Leu Glu Pro Leu Asn Phe Pro Asp Pro Glu Tyr Lys Glu
                165                 170                 175

Glu Glu Glu Asp Gln Asp Ile Gln Gly Glu Ile Ser His Pro Asp Gly
            180                 185                 190

Lys Val Glu Lys Val Tyr Lys Asn Gly Cys Arg Val Ile Leu Phe Pro
        195                 200                 205

Asn Gly Thr Arg Lys Glu Val Ser Ala Asp Gly Lys Thr Ile Thr Val
    210                 215                 220

Thr Phe Phe Asn Gly Asp Val Lys Gln Val Met Pro Asp Gln Arg Val
225                 230                 235                 240

Ile Tyr Tyr Tyr Ala Ala Ala Gln Thr Thr His Thr Thr Tyr Pro Glu
                245                 250                 255

Gly Leu Glu Val Leu His Phe Ser Ser Gly Gln Ile Glu Lys His Tyr
            260                 265                 270

Pro Asp Gly Arg Lys Glu Ile Thr Phe Pro Asp Gln Thr Val Lys Asn
        275                 280                 285

Leu Phe Pro Asp Gly Gln Glu Glu Ser Ile Phe Pro Asp Gly Thr Ile
    290                 295                 300

Val Arg Val Gln Arg Asp Gly Asn Lys Leu Ile Glu Phe Asn Asn Gly
305                 310                 315                 320

Gln Arg Glu Leu His Thr Ala Gln Phe Lys Arg Arg Glu Tyr Pro Asp
                325                 330                 335

Gly Thr Val Lys Thr Val Tyr Ala Asn Gly His Gln Glu Thr Lys Tyr
            340                 345                 350

Arg Ser Gly Arg Ile Arg Val Lys Asp Lys Glu Gly Asn Val Leu Met
        355                 360                 365

Asp Thr Glu Leu
    370
```

<210> 2
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(135)
<223> COOH-terminal peptide from LAP protein

<400> 2
Gln Arg Val Ile Tyr Tyr Tyr Ala Ala Ala Gln Thr Thr His Thr Thr
1 5 10 15

Tyr Pro Glu Gly Leu Glu Val Leu His Phe Ser Ser Gly Gln Ile Glu
20 25 30

Lys His Tyr Pro Asp Gly Arg Lys Glu Ile Thr Phe Pro Asp Gln Thr
35 40 45

Val Lys Asn Leu Phe Pro Asp Gly Gln Glu Glu Ser Ile Phe Pro Asp
50 55 60

Gly Thr Ile Val Arg Val Gln Arg Asp Gly Asn Lys Leu Ile Glu Phe
65 70 75 80

Asn Asn Gly Gln Arg Glu Leu His Thr Ala Gln Phe Lys Arg Arg Glu
85 90 95

Tyr Pro Asp Gly Thr Val Lys Thr Val Tyr Ala Asn Gly His Gln Glu
100 105 110

Thr Lys Tyr Arg Ser Gly Arg Ile Arg Val Lys Asp Lys Glu Gly Asn
115 120 125

Val Leu Met Asp Thr Glu Leu
130 135

<210> 3
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino
acid motif sequence

<220>
<221> misc-feature
<222> (1)..(18)
<223> repeated EP motif

<220>
<221> misc-feature
<222> (1)..(18)
<223> corresponds to EP motifs from human LAG-3 protein

<400> 3
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
1 5 10 15

Glu Pro

<210> 4
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid motif sequence

<220>
<221> misc-feature
<222> (1)..(12)
<223> repeated EP motif

<220>
<221> misc-feature
<222> (1)..(12)
<223> correpsponds to EP motifs from mLAG-3 protein.

<400> 4
Glu Pro Glu Pro Glu Pro Gln Leu Glu Pro Glu Pro
1 5 10

<210> 5
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid motif sequence

<220>
<221> misc-feature
<222> (1)..(23)
<223> repeated EP motif

<220>
<221> misc-feature
<222> (1)..(23)
<223> corresponds to EP motifs from PDGFR protein

<400> 5
Glu Pro Gln Asp Glu Pro Pro Glu Pro Gln Leu Glu Leu Gln Val Glu
1 5 10 15

Pro Glu Pro Glu Leu Glu Gln
20

<210> 6
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic amino acid motif sequence

<220>
<221> misc-feature
<222> (1)..(12)
<223> repeated EP motif

<220>
<221> misc-feature
<222> (1)..(12)
<223> Corresponds to EP motifs from HS1 protein

<400> 6
Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro Glu Pro
1 5 10

<210> 7
<211> 486
<212> PRT
<213> Homo sapiens

<400> 7
Met Trp Lys Ser Val Val Gly His Asp Val Ser Val Ser Val Glu Thr
1 5 10 15

Gln Gly Asp Asp Trp Asp Thr Asp Pro Asp Phe Val Asn Asp Ile Ser
20 25 30

Glu Lys Glu Gln Arg Trp Gly Ala Lys Thr Ile Glu Gly Ser Gly Arg
35 40 45

Thr Glu His Ile Asn Ile His Gln Leu Arg Asn Lys Val Ser Glu Glu
50 55 60

His Asp Val Leu Arg Lys Lys Glu Met Glu Ser Gly Pro Lys Ala Ser
65 70 75 80

His Gly Tyr Gly Gly Arg Phe Gly Val Glu Arg Asp Arg Met Asp Lys
85 90 95

Ser Ala Val Gly His Glu Tyr Val Ala Glu Val Glu Lys His Ser Ser
100 105 110

Gln Thr Asp Ala Ala Lys Gly Phe Gly Gly Lys Tyr Gly Val Glu Arg
115 120 125

Asp Arg Ala Asp Lys Ser Ala Val Gly Phe Asp Tyr Lys Gly Glu Val
130 135 140

Glu Lys His Thr Ser Gln Lys Asp Tyr Ser Arg Gly Phe Gly Gly Arg
145 150 155 160

Tyr Gly Val Glu Lys Asp Lys Trp Asp Lys Ala Ala Leu Gly Tyr Asp
165 170 175

```
Tyr Lys Gly Glu Thr Glu Lys His Glu Ser Gln Arg Asp Tyr Ala Lys
            180                 185                 190

Gly Phe Gly Gly Gln Tyr Gly Ile Gln Lys Asp Arg Val Asp Lys Ser
        195                 200                 205

Ala Val Gly Phe Asn Glu Met Glu Ala Pro Thr Thr Ala Tyr Lys Lys
    210                 215                 220

Thr Thr Pro Ile Glu Ala Ala Ser Ser Gly Ala Arg Gly Leu Lys Ala
225                 230                 235                 240

Lys Phe Glu Ser Met Ala Glu Glu Lys Arg Lys Arg Glu Glu Glu Glu
                245                 250                 255

Lys Ala Gln Gln Val Ala Arg Arg Gln Gln Glu Arg Lys Ala Val Thr
            260                 265                 270

Lys Arg Ser Pro Glu Ala Pro Gln Pro Val Ile Ala Met Glu Glu Pro
        275                 280                 285

Ala Val Pro Ala Pro Leu Pro Lys Lys Ile Ser Ser Glu Ala Trp Pro
    290                 295                 300

Pro Val Gly Thr Pro Pro Ser Ser Glu Ser Glu Pro Val Arg Thr Ser
305                 310                 315                 320

Arg Glu His Pro Val Pro Leu Leu Pro Ile Arg Gln Thr Leu Pro Glu
                325                 330                 335

Asp Asn Glu Glu Pro Pro Ala Leu Pro Pro Arg Thr Leu Glu Gly Leu
            340                 345                 350

Gln Val Glu Glu Glu Pro Val Tyr Glu Ala Glu Pro Glu Pro Glu Pro
        355                 360                 365

Glu Pro Glu Pro Glu Pro Glu Asn Asp Tyr Glu Asp Val Glu Glu Met
    370                 375                 380

Asp Arg His Glu Gln Glu Asp Glu Pro Glu Gly Asp Tyr Glu Glu Val
385                 390                 395                 400

Leu Glu Pro Glu Asp Ser Ser Phe Ser Ser Ala Leu Ala Gly Ser Ser
                405                 410                 415

Gly Cys Pro Ala Gly Ala Gly Ala Gly Ala Val Ala Leu Gly Ile Ser
            420                 425                 430

Ala Val Ala Leu Tyr Asp Tyr Gln Gly Glu Gly Ser Asp Glu Leu Ser
        435                 440                 445

Phe Asp Pro Asp Asp Val Ile Thr Asp Ile Glu Met Val Asp Glu Gly
    450                 455                 460

Trp Trp Arg Gly Arg Cys His Gly His Phe Gly Leu Phe Pro Ala Asn
465                 470                 475                 480
```

Tyr Val Lys Leu Leu Glu
485

<210> 8
<211> 1353
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(1353)
<223> LAP cDNA Open reading frame

<220>
<221> misc_feature
<222> (1186)..(1189)
<223> LAP cDNA translation codon stop

<400> 8
gaaattgcag acttcgaaca acagaaagca aaagaattag ctcgaataga agagtttaaa 60
aaggaggaga tgaggaagct acaaaaggaa cgtaaagttt ttgaaaagta tactacagct 120
gcaagaactt ttccagataa aaaggaacgt gaagaaatac agactttaaa acagcaaata 180
gcagatttac gggaagattt gaaaagaaag gaaaccaaat ggtcaagtac acacagccgt 240
ctcagaagcc agatacaaat gttagtcaga gagaacacag acctccggga agaaataaaa 300
gtgatggaaa gattccgact ggatgcctgg aagagagcag aagccataga gagcagcctc 360
gaggtggaga agaaggacaa gcttgcgaac acatctgttc gatttcaaaa cagtcagatt 420
tcttcaggaa cccaggtaga aaaatacaag aaaaattatc ttccaatgca aggcaatcca 480
cctcgaagat ccaagtctgc acctcctcgt gatttaggca atttggataa gggacaagct 540
gcctctccca gggagccact tgaaccactg aacttcccag atcctgaata taaagaggag 600
gaggaagacc aagacataca gggagaaatc agtcatcctg atggaaaggt ggaaaaggtt 660
tataagaatg ggtgccgtgt tatactgttt cccaatggaa ctcgaaagga agtgagtgca 720
gatgggaaga ccatcactgt cactttcttt aatggtgacg tgaagcaggt catgccagac 780
caaagagtga tctactacta tgcagctgcc cagaccactc acacgacata cccggaggga 840
ctggaagtct tacatttctc aagtggacaa atagaaaaac attacccaga tggaagaaaa 900
gaaatcacgt ttcctgacca gactgttaaa aacttatttc ctgatggaca agaagaaagc 960
attttcccag atggtacaat tgtcagagta caacgtgatg gcaacaaact catagagttt 1020
aataatggcc aaagagaact acatactgcc cagttcaaga gacgggaata cccagatggc 1080
actgttaaaa ccgtatatgc aaacggtcat caagaaacga agtacagatc cggtcggata 1140
agagttaagg acaaggaggg taatgtgcta atggacacgg agctgtgacg atcctcatgt 1200
gatcatgaag taacagtaac tgacttttta tgttaaaaaa tgtacattta ctgtggattc 1260
tgtttaattt attgtgtatg tgtggggaaa agattggatt ctaaaataaa agtttaccct 1320
gtggcatctt catttttata ttctttgaaa tgc 1353

<210> 9
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> misc-feature
<222> (1)..(17)
<223> LAP derived peptide, contains LAP epitope to raise specific LAP antibodies

<400> 9
Ser Pro Arg Glu Pro Leu Glu Pro Leu Asn Phe Pro Asp Pro Glu Tyr
1 5 10 15

Lys

<210> 10
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic fusion protein

<400> 10
Ser Gln Leu Val Leu Leu Leu Glu Arg Leu Leu Gly Glu Gly Tyr Lys
1 5 10 15

Lys Lys Tyr Gln Gln Val Asp Glu Glu Phe Leu Arg Ser Asp His Pro
20 25 30

Ala Ile Leu Arg Ser Gln Ala Arg Leu Pro Gly Phe His Gly Leu Arg
35 40 45

Ser Pro Asp Thr Ser Ser Val Leu Tyr Thr Val Gln Pro Asn Glu Gly
50 55 60

Asp Asn Asp Tyr Ile Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala
65 70 75 80

Asp Glu Gly Pro Leu Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu
85 90 95

Asn Glu Val Asn Thr Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu
100 105 110

Pro Gln Asp Glu Pro Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro
115 120 125

Glu Pro Glu Leu Glu Gln Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg
130 135 140

Ala Glu Ala Glu Asp Ser Phe Leu
145 150